



Integrative Cancer Research Special Interest Group Teleconference

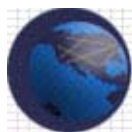
Proteomics SIG Meeting Minutes

Date, Time & Location:	June 21, 2004 11:00 – 12:00 EDT
Attendees:	Greg Bloom – Moffitt Steve Enkemann – Moffitt Steve Eschrich - Moffitt James Lyons-Weiler - University of Pittsburgh Cancer Institute Michael Becich - University of Pittsburgh Cancer Institute Jomol Mathew – New York University School of Medicine Patrick McConnell - Duke University Simon Lin – Duke University Michael Ochs - Fox Chase Cancer Center Alexander Schilling - University of Chicago Reetu Deu - BAH Juli Klemm - BAH
Introduction:	<u>Roll-call, open meeting, review meeting goals</u> <ul style="list-style-type: none">- Review of last meeting- Review mission statement- Review Developer/Adopter activities- Identify and define future activities/research areas
Review Discussions:	<u>Review discussion of last meeting</u> <ul style="list-style-type: none">- Reviewed proteomics technologies in use by the cancer centers. These include 2D gels, MALDI-TOF, SELDI-TOF, and lysate protein arrays.- Data integration: Linking protein expression data with transcript data was cited as a key interest.- Emerging standards: MIAPE, being developed by HUPO, may be emerging as the lead in this area. <u>Review of Mission Statement</u> <ul style="list-style-type: none">- The group reviewed the Mission Statement. Jim Lyons-Weiler suggested adding that the group will coordinate and collaborate with other initiatives including EDRN and caProteo.- Mission Statement will be posted in the next few weeks on the caBIG website <u>Review of Developer/Adopter activities</u> <ul style="list-style-type: none">- Juli has been contacting centers individually and has discussed resources and timelines with each center as part of the matchmaking process. There are verbal understandings of the projects to be undertaken and developer/adopter pairings for these. This process has been focused on funded efforts/interests, but unfunded Adopter roles are highly encouraged.- ProteomicsLIMS: Fox Chase is the Developer center for this project and will work with Moffitt as the Adopter.- Q5: Dartmouth is the Developer of this program, which is aimed at the identification of biomarkers for cancer using MALDI-TOF data. The Institute for Cancer Prevention and NYU are the interested Adopter centers. Both Adopter



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	<p>centers are looking to identify data sets to use in testing. NYU plans to have information by the end of the week. The group requested that there be a demo of this project in an upcoming meeting.</p> <ul style="list-style-type: none">- RProteomics: Duke is the developer of this program whose objective is to process MALDI-TOF and SELDI-TOF data. Interested Adopter centers are Oregon Health, Penn and NYU.- NCI-60 data sets: The Center for Cancer Research has offered to share out data collected on the NCI-60 cell lines. The data available is diverse and includes microarray data, protein lysate array data and SNP data, among others.
Future Activities	<p><u>Future meetings</u></p> <p>The group determined that the following topics should be discussed in future meetings:</p> <ul style="list-style-type: none">- Demos<ul style="list-style-type: none">o There was common interest in a near-term demo of Q5.o The appropriate timing for a presentation of the ProteomicsLIMS project will be determined following discussions between Fox Chase and Moffitt. Steve Enkemann from Moffitt suggested that this could be a project milestone.o Juli will follow-up with Simon Lin and Patrick McConnell regarding the timing of an RProteomics presentation to the group.- Project lead status updates once project activities are underway.- Common data element creation and vocabulary identification (key activity)<ul style="list-style-type: none">o Juli introduced the idea of a liaison for CDE creation. The liaison will work with project groups to determine data elements, then coordinate with NCI to create the given data elements. A SOW will likely be issued for this effort<ul style="list-style-type: none">▪ Jim Lyons-Weiler mentioned that Tina Xiao of the Cal Tech Jet Propulsion Laboratory has made significant progress on the creation of proteomics CDEs.o Creation of UML models that can be loaded directly into the caDSR is the preferred route for CDE creation.- Other areas of research or discussion<ul style="list-style-type: none">o Proteomics standards – Keep abreast of developments with MIAPE via Lianhong (Vanderbilt).o Analysis integration – Keep abreast of how disparate data types are analyzed in conjunction with another- The group was encouraged to review the caBIG Compatibility Document and focus on the Silver level of compatibility for this year's development efforts.
Other Items Discussed	<p>caProteo: Jim Lyons-Weiler gave an overview of the caProteo effort and how it relates to caBIG</p> <ul style="list-style-type: none">o Purpose: Allow informaticians at distant sites to work together on a common bioinformatics analysis solution aimed at optimizing biomarker discovery in peptide time-of-flight profiles.o Current group involves members of the EDRN community and the caBIG



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community.

- caProteo is currently running multi-site validation studies (some publicly available, some not as they are still in their preliminary phases)
- caProteo is in the needs development phase, no tool development has taken place
- Areas of similarity between caProteo and the Proteomics SIG include: implementing paradigms enabling proper study designs for proteomics, statistical modeling, lab tools, laboratory workflow, data characterization
- It may be possible for interested centers to become associate members of EDRN
- A whitepaper describing the goals of caProteo is being crafted. An outline of the paper was created by 8-9 sites related to the EDRN effort. These sites include: Duke, George Washington University, University of Alabama Birmingham, Texas A&M and Jackson Laboratories. Jim will send a copy of the outline to the group to solicit contributions for the white paper

Next meeting will be on Monday, July 12, 2pm

- Update on Project activities
- EDRN opportunities
- Presentations – To be determined

Action Items:

Name Responsible	Action Item	Date Due	Notes
Juli Klemm	Follow up with Dartmouth regarding Q5 demonstration	6/25/04	
Jim Lyons-Weiler	Send caProteo white paper outline to SIG participants to solicit input	6/23/04	
Juli Klemm/Jim Lyons-Weiler	Coordinate a conversation with Tina Xiao about proteomics CDEs	6/25/04	
Juli Klemm	Send Alex Schilling the caBIG Compatibility Guidelines document	6/21/04	
Juli Klemm	Follow up with Simon Lin and Patrick McConnell regarding an RProteomics presentation	6/25/04	
Juli Klemm	Distribute meeting minutes and updates to the Mission Statement	6/25/04	